

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: FORSBERG, ET AL. § Docket No.: P02188US0
Serial No.: NOT YET ASSIGNED § Examiner:
Filing Date: 07/06/2001 § Art Unit:
Title: A NOVEL ENGINEERED §
SUPERANTIGEN FOR HUMAN §
THERAPY §

Box Sequence Listing
Assistant Commissioner for Patents
Washington, D.C. 20231

SEQUENCE LISTING 37 CFR 1.821

Dear Sir:

In compliance with 37 CFR 1.821, Applicants submit the attached sequence listing and provide one enclosed 3.5 inch disk. The file is stored as Seq.txt.

I hereby state that the content of the paper and computer readable copies of the sequence listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively, are the same.

Applicant believes that there is no additional fee required to file this paper. If Applicant is in error, the Commissioner is hereby authorized to charge any required fees and/or credits by this paper and during the entire pendency of this application to Account No. 06-2375/10104199.

July 6, 2001

Respectfully submitted,



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SEQUENCE LISTING

<110> FORSBERG, GORAN
ERLANDSSON, EVA
ANTONSSON, PER
WALSE, BJORN

<120> A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

<130> P02188US0;10104199

<140> TBA
<141> 2001-06-20

<160> 7

<170> PatentIn version 3.0

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<211> 672
<212> PRT
<213> Artificial Sequence

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<221> PEPTIDE
<222> (1)..(672)
<223> Conjugate protein

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Tyr Met His Trp Val Lys Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Asn Pro Asn Asn Gly Val Thr Leu Tyr Asn Gln Lys Phe
50 55 60

Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Met Ile Thr Asn Tyr Val Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
115 120 125

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
130 135 140

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
145 150 155 160

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
 180 185 190
 Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala
 195 200 205
 Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg Asp Ser Gly Gly
 210 215 220
 Pro Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys
 225 230 235 240
 Ser Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr
 245 250 255
 Tyr Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe
 260 265 270
 Leu Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp
 275 280 285
 Tyr Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu
 290 295 300
 Tyr Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln
 305 310 315 320
 Cys Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Val
 325 330 335
 Thr Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile
 340 345 350
 Asn Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val
 355 360 365
 Lys Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala
 370 375 380
 Arg His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe
 385 390 395 400
 Gly Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly
 405 410 415
 Ser Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp
 420 425 430
 Thr Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser
 435 440 445
 Leu Ser Ile Ser Leu Tyr Leu Tyr Thr Thr Ser Ile Val Met Thr Gln
 450 455 460
 Thr Pro Thr Ser Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr
 465 470 475 480
 Cys Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln

485 490 495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Thr Ser Ser Arg
500 505 510

Tyr Ala Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Tyr Gly Thr Asp
515 520 525

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Ala Ala Val Tyr
530 535 540

Phe Cys Gln Gln Asp Tyr Asn Ser Pro Pro Thr Phe Gly Gly Gly Thr
545 550 555 560

Lys Leu Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe
565 570 575

Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys
580 585 590

Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile
595 600 605

Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln
610 615 620

Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr
625 630 635 640

Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His
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Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Ser
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Asn Ser Lys Ala Ile Thr Ser Ser Glu Lys Ser Ala Asp Gln Phe Leu
35 40 45

Thr Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Thr Ala Ala Thr Ser Glu Tyr

65 70 75 80

Glu Gly Ser Ser Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
 85 90 95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
 100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
 115 120 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
 130 135 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
 145 150 155 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
 165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
 180 185 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
 195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Thr Thr Ile Ser Ser Thr Ser Leu
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Ser Ile Ser Leu Tyr Leu Tyr Thr Thr
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 20 25 30

Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu
 35 40 45

Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
 50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr
 65 70 75 80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys

85	90	95	
Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr			
100	105	110	
Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn			
115	120	125	
Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys			
130	135	140	
Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg			
145	150	155	160
His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly			
165	170	175	
Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser			
180	185	190	
Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr			
195	200	205	
Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu			
210	215	220	
His Ile Ala Leu Tyr Leu Tyr Thr Thr			
225	230		
<210> 4			
<211> 233			
<212> PRT			
<213> Staphylococcus sp.			
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Glu Leu Gln Gly Thr Ala Leu Gly Asn Leu Lys Gln Ile Tyr Tyr Tyr			
20	25	30	
Asn Glu Lys Ala Lys Thr Glu Asn Lys Glu Ser His Asp Gln Phe Leu			
35	40	45	
Gln His Thr Ile Leu Phe Lys Gly Phe Phe Thr Asp His Ser Trp Tyr			
50	55	60	
Asn Asp Leu Leu Val Asp Phe Asp Ser Lys Asp Ile Val Asp Lys Tyr			
65	70	75	80
Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys			
85	90	95	
Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr			
100	105	110	
Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn			
115	120	125	
Leu Trp Leu Asp Gly Lys Gln Asn Thr Val Pro Leu Glu Thr Val Lys			

130 135 140
 Thr Asn Lys Lys Asn Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
 145 150 155 160
 Arg Tyr Leu Gln Glu Lys Tyr Asn Leu Tyr Asn Ser Asp Val Phe Asp
 165 170 175
 Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Thr Ser Thr Glu Pro
 180 185 190
 Ser Val Asn Tyr Asp Leu Phe Gly Ala Gln Gly Gln Tyr Ser Asn Thr
 195 200 205
 Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Met
 210 215 220
 His Ile Asp Ile Tyr Leu Tyr Thr Ser
 225 230
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 <211> 203
 <212> PRT
 <213> Staphylococcus sp.
 <400> 5
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 1 5 10 15
 Lys His Ser Tyr Ala Asp Ala Asn Pro Ile Ile Gly Ala Asn Lys Ser
 20 25 30
 Thr Gly Asp Gln Phe Leu Glu Asn Thr Leu Leu Tyr Lys Ala Phe Phe
 35 40 45
 Leu Leu Ile Asn Phe Asn Ser Ala Glu Met Ala Gln His Phe Lys Ser
 50 55 60
 Lys Asn Val Asp Val Tyr Ala Ile Arg Tyr Ala Ala Ala Cys Arg Thr
 65 70 75 80
 Ala Cys Thr Tyr Gly Val Thr Pro His Ala Gly Asn Ala Leu Lys
 85 90 95
 Ala Arg Lys Lys Ile Pro Ile Asn Leu Trp Ile Ile Gly Val Gln Lys
 100 105 110
 Glu Val Ser Leu Asp Lys Val Gln Thr Asp Lys Lys Asn Val Thr Val
 115 120 125
 Gln Glu Leu Asp Ala Gln Ala Arg Arg Tyr Leu Gln Lys Asp Leu Lys
 130 135 140
 Leu Tyr Asn Ala Ile Gln Arg Gly Lys Leu Glu Phe Asp Ser Ala Ala
 145 150 155 160
 Ala Ser Lys Val Ser Tyr Asp Leu Phe Asp Val Ala Gly Asp Phe Pro
 165 170 175
 Glu Lys Gln Leu Arg Ile Tyr Ser Asp Asn Lys Thr Leu Ser Thr Glu

DRAFT RELEASE SOURCE

180

185

190

His Leu His Ile Asp Ile Tyr Leu Tyr Glu Ala
195 200

<210> 6
<211> 217
<212> PRT
<213> Staphylococcus sp.

<400> 6

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1 5 10 15

Ala Tyr Gly Gln Tyr Asn His Pro Phe Ile Lys Glu Asn Ile Lys Ser
20 25 30

Asp Glu Ile Ser Gly Glu Lys Asp Leu Ile Phe Arg Asn Gln Gly Asp
35 40 45

Ser Gly Asn Asp Leu Arg Val Lys Phe Ala Thr Ala Asp Leu Ala Gln
50 55 60

Lys Phe Lys Asn Lys Asn Val Asp Ile Tyr Gly Ala Ser Phe Tyr Tyr
65 70 75 80

Lys Cys Glu Lys Ile Ser Glu Asn Ile Ser Glu Cys Leu Tyr Gly Gly
85 90 95

Thr Thr Leu Asn Ser Glu Lys Leu Ala Gln Glu Arg Val Ile Gly Ala
100 105 110

Asn Val Trp Val Asp Gly Ile Gln Lys Glu Thr Glu Leu Ile Arg Thr
115 120 125

Asn Lys Lys Asn Val Thr Leu Gln Glu Leu Asp Ile Lys Ile Arg Lys
130 135 140

Ile Leu Ser Asp Lys Tyr Lys Ile Tyr Tyr Lys Asp Ser Glu Ile Ser
145 150 155 160

Lys Gly Leu Ile Glu Phe Asp Met Lys Thr Pro Arg Asp Tyr Ser Phe
165 170 175

Asp Ile Tyr Asp Leu Lys Gly Glu Asn Asp Tyr Glu Ile Asp Lys Ile
180 185 190

Tyr Glu Asp Asn Lys Thr Leu Lys Ser Asp Asp Ile Ser His Ile Asp
195 200 205

Val Asn Leu Tyr Thr Lys Lys Lys Val
210 215

<210> 7
<211> 233
<212> PRT
<213> Staphylococcus sp.

<400> 7

Ser Glu Lys Ser Glu Glu Ile Asn Glu Lys Asp Leu Arg Lys Lys Ser
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Glu Leu Gln Arg Asn Ala Leu Ser Asn Leu Arg Gln Ile Tyr Tyr Tyr
20 25 30

Asn Glu Lys Ala Ile Thr Glu Asn Lys Glu Ser Asp Asp Gln Phe Leu
35 40 45

Glu Asn Thr Leu Leu Phe Lys Gly Phe Phe Thr Gly His Pro Trp Tyr
50 55 60

Asn Asp Leu Leu Val Asp Leu Gly Ser Lys Asp Ala Thr Asn Lys Tyr
65 70 75 80

Lys Gly Lys Lys Val Asp Leu Tyr Gly Ala Tyr Tyr Gly Tyr Gln Cys
85 90 95

Ala Gly Gly Thr Pro Asn Lys Thr Ala Cys Met Tyr Gly Gly Val Thr
100 105 110

Leu His Asp Asn Asn Arg Leu Thr Glu Glu Lys Lys Val Pro Ile Asn
115 120 125

Leu Trp Ile Asp Gly Lys Gln Thr Thr Val Pro Ile Asp Lys Val Lys
130 135 140

Thr Ser Lys Lys Glu Val Thr Val Gln Glu Leu Asp Leu Gln Ala Arg
145 150 155 160

His Tyr Leu His Gly Lys Phe Gly Leu Tyr Asn Ser Asp Ser Phe Gly
165 170 175

Gly Lys Val Gln Arg Gly Leu Ile Val Phe His Ser Ser Glu Gly Ser
180 185 190

Thr Val Ser Tyr Asp Leu Phe Asp Ala Gln Gly Gln Tyr Pro Asp Thr
195 200 205

Leu Leu Arg Ile Tyr Arg Asp Asn Lys Thr Ile Asn Ser Glu Asn Leu
210 215 220

His Ile Asp Leu Tyr Leu Tyr Thr Thr
225 230